Spread of a contagion in a heterogeneous population-
Linear algebra tutorial

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1 Geometric growth

In the simplest model, suppose that every infected person meets \( m \) people per day (on average) and each such meeting yields a virus transmission with probability \( p \). Moreover, suppose every infected person recovers (or is otherwise removed from the infectious set) with probability \( \alpha \) each day. In a population of size \( N \), let

\[
I_t = \{ \text{The number of infected individuals on day } t \}
\]

Then ignoring random fluctuations and denoting \( \beta = pm \),

\[
I_{t+1} = I_t + \beta I_t - \alpha I_t = I_t(1 + \gamma)
\]

where \( \gamma = \beta - \alpha \).

Despite its extreme simplicity, this formula often represents initial growth of epidemics quite well. The factor \( 1 + \gamma \) is often denoted \( r_0 \). If \( \gamma > 0 \) the epidemic grows exponentially, while if \( \gamma < 0 \) it decays.

2 Heterogeneous populations

Suppose we consider two communities. In the first the contagion has spread widely and is now shrinking due to effective mitigation (e.g. lockdown), with \( I_0 = 10^4 \), \( I_{t+1} = 0.9 \cdot I_t \). In the second community, the contagion is much smaller but growing rapidly: \( I_0 = 10 \), \( I_{t+1} = 2I_t \).

If these two communities are considered together, the situation may look rosy in the first few days, but can get much worse later. A plot with these parameters can be found in Figure 2; note the total number of people infected decreases in the first six days but starts increasing afterwards.

A more complex situation arises when multiple types of individuals interact. For a concrete example, suppose that a fraction \( \theta \) of the population are cashiers and the rest are customers.
Every cashier interacts, on average, with $m_1$ customers and with one other cashier per day. Every customer interacts, on average, with $m_2$ cashiers and one other customer per day. Naturally, $m_1 > 1 > m_2$. Moreover, counting the expected number of customer-cashier interactions per day shows that

$$\theta m_1 = (1 - \theta)m_2$$  (2)

Each interaction between an infected person and a susceptible one yields transmission with probability $p$. For specific values, suppose that $\theta = 1/161, m_1 = 40, m_2 = 1/4$, and $p = 1/10$, so (2) holds. We also assume that every infected person is removed (recovered or quarantined) with probability $\alpha$ (say with $\alpha = 1/5$).

Denote by $I_t$ the number of infected customers and by $J_t$ the number of infected cashiers. Suppose initially that $I_0 = 100$ and $J_0 = 0$. The next plot shows the numbers $I_t$ and $J_t$ over a period of 10 days.

In the early phases of the epidemic, the number of susceptibles hardly changes. So on average,

$$I_{t+1} = I_t + p \cdot (I_t + m_1 J_t) - \alpha I_t$$
$$J_{t+1} = J_t + p \cdot (J_t + m_2 I_t) - \alpha J_t$$  (4)

How does this contagion spread? Consider the numerical example in (3), where $\alpha = 1/5$. During the five days (on average) that a customer is contagious, they will interact (on average) with 25/4 people and infect in expectation $25p/4 = 5/8$ people. For a cashier, the corresponding number is 101/2.
Figure 2: The X axis denotes the time and the Y axis the number of people infected each day, where red shows the number of infected customers ($I_t$) and blue the number of infected cashiers ($J_t$).

Figure 3: The X axis denotes the time and the Y axis the risk in the early stage of the epidemic for customers (in red) and for cashiers (in green).

Since cashiers comprise only $\theta = 1/401$ of the population, naive averaging would yield that the expected number of people an infected person would infect is

$$\frac{400}{401} \cdot \frac{5}{8} + \frac{1}{401} \cdot \frac{101}{2} < 0.75,$$

which suggests the contagion is shrinking.

However, this heuristic is faulty. Rewriting (4) in matrix form, we have

$$\begin{pmatrix} I_{t+1} \\ J_{t+1} \end{pmatrix} = A \begin{pmatrix} I_t \\ J_t \end{pmatrix}$$
where

\[ A = \begin{pmatrix} \frac{9}{10} & 10 \\ \frac{1}{40} & \frac{9}{10} \end{pmatrix} \]  

(5)

We deduce that

\[ \begin{pmatrix} I_t \\ J_t \end{pmatrix} = A^t \begin{pmatrix} I_0 \\ J_0 \end{pmatrix} \]

To compute the powers of \( A^t \) we diagonalize \( A \). First find eigenvalues and eigenvectors by solving \( Av = \lambda v \), that is

\[
\begin{cases}
\frac{9v_1}{10} + 10v_2 = \lambda v_1 \\
v_1 + \frac{9v_2}{10} = \lambda v_2
\end{cases}
\]

Equivalently,

\[
\begin{cases}
10v_2 = (\lambda - \frac{9}{10})v_1 \\
v_1 = (\lambda - \frac{9}{10})v_2
\end{cases}
\]

Multiplying these equations gives that \( 1/4 = (\lambda - 9/10)^2 \), so \( \lambda \in \{7/5, 2/5\} \).

For \( \lambda = 7/5 \) we get \( v = \begin{pmatrix} 20 \\ 1 \end{pmatrix} \); for \( \tilde{\lambda} = 2/5 \), we get \( \tilde{v} = \begin{pmatrix} -20 \\ 1 \end{pmatrix} \).

Represent

\[ \begin{pmatrix} I_0 \\ J_0 \end{pmatrix} = \begin{pmatrix} 100 \\ 0 \end{pmatrix} = \frac{5}{2}(v - \tilde{v}) \]

Thus

\[ \begin{pmatrix} I_t \\ J_t \end{pmatrix} = \frac{5}{2}A^t(v - \tilde{v}) = \frac{5}{2}\left[ \left( \frac{7}{5} \right)^t v - \left( \frac{2}{5} \right)^t \tilde{v} \right] \]  

(6)

The first summand grows exponentially in \( t \), while the second shrinks. So the infection grows with growth factor 7/5.

### 3 Introducing the SIR model

In a population of size \( N \), write

\[ S_t = \{ \text{The number of susceptible individuals on day } t \} \]
\[ I_t = \{ \text{The number of infected individuals on day } t \} \]
\[ R_t = \{ \text{The number of removed individuals on day } t \} \]

Here, removed can indicate recovery or showing symptoms that lead to quarantine, so an individual cannot infect others.
Suppose each infected person meets \( m \) people each day, on average, and a fraction \( p \) of these meetings result in transmission of the infection. Moreover, each infected person is removed with probability \( \alpha \) each day. Then, with \( \beta = mp \), we have

\[
S_{t+1} = S_t - \frac{\beta}{N} S_t I_t
\]
\[
I_{t+1} = I_t + \frac{\beta}{N} S_t I_t - \alpha I_t
\]
\[
R_{t+1} = R_t + \alpha I_t
\]

This is the celebrated SIR model [1].

In the early stages of the infection, \( S_t/N \) is close to 1, so equation (7) for \( I_{t+1} \) is close to the geometric sequence \( I_{t+1} = (1 + \gamma)I_t \), where \( \gamma = \beta - \alpha \).

References